We claim:

1. A substantially purified nucleic acid molecule that encodes a maize or soybean tetrapyrrole pathway enzyme or fragment thereof, wherein said maize or soybean tetrapyrrole pathway enzyme is selected from the group consisting of:

(a) putative chlorophyll synthetase enzyme;

(b) protochlorophyllide reductase enzyme;

(c) putative protochlorophyllide reductase enzyme;

(d) coproporhyrinogen oxidase enzyme;

(e) protoporphyringogen oxidase enzyme;

(f) uroporphyrinogen decarboxylase enzyme;

(g) putative uroporphyrinogen decarboxylase enzyme;

(h) porphobilinogen synthase enzyme;

(i) hydroxymethylbilane synthase enzyme;

(j) glutamate-1-semialdehyde 2,1-aminomutase enzyme;

(k) glutamate tRNA ligase enzyme;

(l) glutamyl-tRNA reductase enzyme;

(m) Mg-chelatase enzyme; and

(n) ferrochelatase enzyme.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 677.

3. A substantially purified maize or soybean tetrapyrrole enzyme or fragment thereof, wherein said maize or soybean tetrapyrrole pathway enzyme is selected from the group consisting of

(a) putative chlorophyll synthetase enzyme or fragment thereof;

(b) protochlorophyllide reductase enzyme or fragment thereof;

(c) putative protochlorophyllide reductase enzyme or fragment thereof;

(d) coproporhyrinogen oxidase enzyme or fragment thereof;

(e) protoporphyringogen oxidase enzyme or fragment thereof;

(f) uroporphyrinogen decarboxylase enzyme or fragment thereof;

(g) putative uroporphyrinogen decarboxylase enzyme or fragment thereof;

(h) porphobilinogen synthase enzyme or fragment thereof;

(i) hydroxymethylbilane synthase enzyme or fragment thereof;

(j) glutamate-1-semialdehyde 2,1-aminomutase enzyme or fragment thereof;

(k) glutamate tRNA ligase enzyme or fragment thereof;

(l) glutamyl-tRNA reductase enzyme or fragment thereof;

(m) Mg-chelatase enzyme or fragment thereof; and

(n) ferrochelatase enzyme or fragment thereof.

4. A substantially purified maize or soybean or tetrapyrrole pathway enzyme or fragment thereof according to claim 3, wherein said maize or soybean tetrapyrrole enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of consisting of SEQ ID NO: 1 through SEQ ID NO: 677.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean tetrapyrrole pathway or enzyme or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a putative chlorophyll synthetase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a protochlorophyllide reductase enzyme or fragment thereof;

(c) a nucleic acid sequence which encodes for a putative protochlorophyllide reductase enzyme or fragmen thereof;

(d) a nucleic acid sequence which encodes for a coproporhyrinogen oxidase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a protoporphyringogen oxidase enzyme or fragment thereof;

(f) a nucleic acid sequence which encodes for an uroporphyrinogen decarboxylase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for a putative uroporphyrinogen decarboxylase enzyme or fragment thereof

(h) a nucleic acid sequence which encodes for a porphobilinogen synthase enzyme of fragment thereof;

(i) a nucleic acid sequence which encodes for a hydroxymethylbilane synthase enzyme or fragment thereof;

(j) a nucleic acid sequence which encodes for a glutamate-1-semialdehyde 2,1-aminomutase enzyme oor fragment thereof;

(k) a nucleic acid sequence which encodes a glutamate tRNA ligase enzyme or fragment thereof;

(l) a nucleic acid sequence which encodes a glutamyl-tRNA reductase enzyme or fragment thereof;

(m) a nucleic acid sequence which encodes a Mg-chelatase enzyme or fragment thereof;

(n) a nucleic acid seqence which encodes a ferrochelatase enzyme or fragment thereof;

(o) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (n); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (l).

8. A method for determining a level or pattern in a plant cell of an transcription factor in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 677 or compliments thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary

nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said transcription factor;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said transcription factor in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.